

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 28, 2002, 17:25:59 ; Search time 37.53 Seconds
(without alignments)
576.075 Million cell updates/sec

Title: US-09-502-984B-1

Perfect score: 1194

Sequence: 1 APPPNLPDPKFEKALIAA.....GGFWSAMSEPSILTPSDLD 225

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR_71:*
2: PIR1:*
3: PIR2:*
4: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	1194	100.0	508 1 ZUHUR	erythropoietin rec
2	982.5	82.3	507 1 A32385	erythropoietin rec
3	981.5	82.2	507 1 A46713	erythropoietin rec
4	966.5	80.9	265 2 S14081	erythropoietin rec
5	205	17.2	625 2 S35317	hematopoietic grow
6	198	16.6	626 2 S37622	proto-oncogene - m
7	185	15.5	579 2 B45266	MPL-K protein prec
8	185	15.5	635 2 A45266	MPL-K protein prec
9	159	13.3	581 2 I45971	prolactin receptor
10	148	12.4	616 2 A30304	prolactin receptor
11	144.5	12.1	831 2 J01655	prolactin receptor
12	136.5	11.4	830 2 I50455	prolactin receptor
13	128	10.7	288 2 B59405	prolactin receptor
14	128	10.7	376 2 A59405	prolactin receptor
15	128	10.7	622 2 A40144	prolactin receptor
16	126	10.6	292 2 I77525	prolactin receptor
17	126	10.6	303 2 I77524	prolactin receptor
18	126	10.6	522 2 B45268	interleukin-9 rece
19	126	10.6	608 2 I53269	prolactin receptor
20	123.5	10.3	677 2 S33608	somatotropin-bindi
21	121.5	10.2	634 2 S33339	somatotropin recep
22	121	10.1	310 2 A29884	prolactin receptor
23	121	10.1	412 2 A41070	prolactin receptor
24	121	10.1	610 2 A34631	lactogen receptor
25	121	10.1	610 2 A36116	prolactin receptor
26	117.5	9.8	638 2 S12136	somatotropin recep
27	117	9.8	608 2 S32823	somatotropin recep
28	116.5	9.8	638 2 B28176	somatotropin recep
29	116	9.7	897 1 A39255	cytokine receptor

30	113	9.5	630 2 I51086	prolactin receptor
31	111.5	9.3	1097 2 S17308	leukemia inhibitor
32	108.5	9.1	279 2 B32985	somatotropin-bindi
33	108.5	9.1	467 2 I56896	gene gfi-2 protein
34	108.5	9.1	638 2 A33505	somatotropin recep
35	108	9.0	976 2 A6355	protein-tyrosine k
36	108	9.0	1825 2 C88400	protein H19M22.1 l
37	108	9.0	1825 2 T32828	hypothetical prote
38	107	9.0	468 2 A40256	interleukin-3 rece
39	106.5	8.9	378 2 A40256	interleukin-3 rece
40	105.5	8.8	975 2 I48974	receptor-protein t
41	104	8.7	2594 2 A35774	kinase-related pro
42	102	8.5	896 1 A35782	cytokine receptor
43	101	8.5	917 2 S49004	tyrosine kinase Mp
44	100.5	8.4	917 2 I49639	glycoprotein 130 -
45	99	8.3	1863 2 S46217	protein-tyrosine-p

ALIGNMENTS

RESULT 1

ZUHUR

erythropoietin receptor precursor - human

C:Species: Homo sapiens (man)

C:Date: 12-Feb-1993 #sequence revision 05-Apr-1995 #text change 22-Jun-1999

C:Accession: A43799; A60160; A49824; A53958; A55280; I52563

R:Jones, S.S.; D'Andrea, A.D.; Haines, L.L.; Wong, G.G.

Blood 76, 31-35, 1990

A:Title: Human erythropoietin receptor: cloning, expression, and biologic characteriz

A:Reference number: A43799; MUID:90304340

A:Accession: A43799

A:Molecule type: mRNA

A:Residues: 1-508 <JUN>

A:Cross-references: GB:M60459; NID:g182244; PIDN:AAA52403.1; PID:g182245

R:Winkelmann, J.C.; Penny, L.A.; Deaven, L.L.; Forget, B.G.; Jenkins, R.B.

Blood 76, 24-30, 1990

A:Title: The gene for the human erythropoietin receptor: analysis of the coding seque

A:Reference number: A60160; MUID:90304334

A:Accession: A60160

A:Status: not compared with conceptual translation

A:Molecule type: mRNA; DNA

A:Residues: 1-101, 'R', 103-188, 'R', 191-243, 'E', 245-508 <WIN>

R:Nozuchi, C.T.; Bae, K.S.; Chih, K.; Wada, Y.; Schechter, A.N.; Hankins, W.D.

Blood 78, 2548-2556, 1991

A:Title: Cloning of the human erythropoietin receptor gene.

A:Reference number: A49824; MUID:92399733

A:Accession: A49824

A:Molecule type: DNA

A:Residues: 1-508 <NOG>

A:Cross-references: GB:S45332; NID:g255496; PIDN:AAA23271.1; PID:g255497

A:Experimental source: Placenta

A:Note: Sequence extracted from NCBI backbone (NCBIN:113293, NCBIPI:113294)

R:Ehrenman, K.; St. John, T.

Exp. Hematol. 19, 973-977, 1991

A:Title: The erythropoietin receptor gene: cloning and identification of multiple tra

A:Reference number: A53958; MUID:91372359

A:Accession: A53958

A:Molecule type: mRNA

A:Residues: 1-508 <EHR>

R:Penny, L.A.; Forget, B.G.

Genomics 11, 974-980, 1991

A:Title: Genomic organization of the human erythropoietin receptor gene.

A:Reference number: A55280; MUID:92147143

A:Accession: A55280

A:Molecule type: DNA

A:Residues: 1-17,381-387, 'LHEQOQDA', 391-395,504-508 <PEN>

A:Note: sequence modified after extraction from NCBI backbone

A:Note: the authors translated the codon GAT for residue 31 as B

R:Mauche, L.; Touramille, C.; Hatlab, C.; Boffa, G.; Cartton, J.P.; Chretien, S.

Blood 78, 2557-2563, 1991

A:Title: Cloning of the gene encoding the human erythropoietin receptor.

A:Reference number: 152563; MUID:92399734
A:Accession: 152563
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-96 <R>
A:Cross-references: GB:M76595; NID:9182147; PIDN:AAA52393.1; PID:9553281
C:Genetics:
A:Gene: GDB:EPOR
A:Cross-references: GDB:125242; OMIM:133171
A:Map position: 19p13.3-19p13.2
A:Introns: 39/1; 84/2; 143/1; 195/3; 247/1; 276/2; 305/3
C:Superfamily: erythropoietin receptor; cytokine receptor; glycoprotein; transmembrane protein
C:Keywords: alternative splicing; cytokine receptor; glycoprotein; transmembrane protein
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-508/Product: erythropoietin receptor #status predicted <MAT>
F:52-350/Domain: extracellular #status predicted <EXT>
F:52-339/Domain: cytokine receptor homology <CRS>
F:233-237/Region: WSXWS motif
F:251-272/Domain: transmembrane #status predicted <TM>
F:273-508/Domain: intracellular #status predicted <INT>
F:52-62; 91-107/Disulfide bonds: #status predicted
F:76/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 1194; DB 1; Length 508;
Best Local Similarity 100.0%; Pred. No. 8.7e-102;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPNPDPKFEKSKAALLAARGPEELCTERLEDCVCFWEERASAGVGNYSFYOLE 60
DB 25 APPNPDPKFEKSKAALLAARGPEELCTERLEDCVCFWEERASAGVGNYSFYOLE 84
QY 61 DEPWKLCRLHQAPTARGAVRFMCSLPTADTSSFPLELRTAASGAPRYHRYHINEVYL 120
DB 85 DEPWKLCRLHQAPTARGAVRFMCSLPTADTSSFPLELRTAASGAPRYHRYHINEVYL 144
QY 121 LDAPVGLVARLADSGHVVLRWLPPEPTMTSHIRYEVDSAGNGAGSVQRYEILEGRTE 180
DB 145 LDAPVGLVARLADSGHVVLRWLPPEPTMTSHIRYEVDSAGNGAGSVQRYEILEGRTE 204
QY 181 CVALSNLGRGRTYFAVARARMAEPFSGFWSAMSEPSLTPSDLD 225
DB 205 CVALSNLGRGRTYFAVARARMAEPFSGFWSAMSEPSLTPSDLD 249

RESULT 2

A32385
erythropoietin receptor precursor, membrane-bound form - mouse
C:Species: Mus musculus (house mouse)
C:Date: 28-Sep-1990 #sequence_revision 05-Apr-1995 #text_change 22-Jun-1999
C:Accession: A41686; A32385; S13249

R:Hino, M.; Tojo, A.; Misawa, Y.; Morii, H.; Takaku, F.; Shibuya, M.
Mol. Cell. Biol. 11, 5527-5533, 1991
A:Title: Unregulated expression of the erythropoietin receptor gene caused by insertion
A:Reference number: A41686; MUID:92017832
A:Accession: A41686

A:Molecule type: mRNA
A:Residues: 1-507 <HIN>
A:Cross-references: GB:S59388; NID:9237036; PIDN:AA820029.1; PID:9237037
A:Experimental source: murine erythroleukemia (MEU) cell line F5-5
R:D Andrea, A.D.; Lodish, H.F.; Wong, G.G.
Cell 57, 277-285, 1989

A:Title: Expression cloning of the murine erythropoietin receptor.
A:Reference number: A32385; MUID:89195238
A:Accession: A32385
A:Molecule type: mRNA
A:Residues: 1-507 <DA>
A:Cross-references: GB:J04843; NID:9193090; PIDN:AAA7571.1; PID:9309219
A:Experimental source: murine erythroleukemia (MEU) cells, subclone 745
J. Mol. Biol. 216, 567-575, 1990

A:Title: Characterization of murine erythropoietin receptor genes.
A:Reference number: S13249; MUID:91080149

A:Accession: S13249
A:Molecule type: mRNA
A:Residues: 1-507 <KUR>
A:Cross-references: EMBL:X53081; NID:950861; PIDN:CAA37248.1; PID:950862
A:Experimental source: murine erythroleukemia K-1 cells
C:Genetics:
A:Introns: 39/1; 83/2; 142/1; 194/3; 246/1; 275/2; 304/3
C:Superfamily: erythropoietin receptor; cytokine receptor; glycoprotein; transmembrane prot
C:Keywords: alternative splicing; cytokine receptor; glycoprotein; transmembrane prot
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-507/Product: erythropoietin receptor #status predicted <MAT>
F:25-249/Domain: extracellular #status predicted <EXT>
F:52-338/Domain: cytokine receptor homology <CRS>
F:250-271/Domain: transmembrane #status predicted <TM>
F:272-507/Domain: intracellular #status predicted <INT>
F:52-62; 90-106/Disulfide bonds: #status predicted
F:75/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 82.3%; Score 962.5; DB 1; Length 507;
Best Local Similarity 83.1%; Pred. No. 2.3e-82;
Matches 187; Conservative 13; Mismatches 24; Indels 1; Gaps 1;

QY 1 APPNPDPKFEKSKAALLAARGPEELCTERLEDCVCFWEERASAGVGNYSFYOLE 60
DB 25 APPNPDPKFEKSKAALLAARGPEELCTERLEDCVCFWEERASAGVGNYSFYOLE 83
QY 61 DEPWKLCRLHQAPTARGAVRFMCSLPTADTSSFPLELRTAASGAPRYHRYHINEVYL 120
DB 84 GDSKSCSLHQAPTARGAVRFMCSLPTADTSSFPLELRTAASGAPRYHRYHINEVYL 143
QY 121 LDAPVGLVARLADSGHVVLRWLPPEPTMTSHIRYEVDSAGNGAGSVQRYEILEGRTE 180
DB 144 LDAPVGLVARLADSGHVVLRWLPPEPTMTSHIRYEVDSAGNGAGSVQRYEILEGRTE 203
QY 181 CVALSNLGRGRTYFAVARARMAEPFSGFWSAMSEPSLTPSDLD 225
DB 204 CVALSNLGRGRTYFAVARARMAEPFSGFWSAMSEPSLTPSDLD 248

RESULT 3

A46713
erythropoietin receptor precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
C:Accession: A46713

R:Masuda, S.; Nagao, M.; Takahata, K.; Konishi, Y.; Gallyas Jr., F.; Tabira, T.; Sasa
J. Biol. Chem. 268, 11208-11216, 1993
A:Title: Functional erythropoietin receptor of the cells with neural characteristics.
A:Reference number: A46713; MUID:9326574
A:Accession: A46713

A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-507 <MAS>
A:Cross-references: GB:D13566; NID:9286209; PIDN:BA02761.1; PID:9286210

A:Experimental source: PC12 and erythroid cells
A:Note: sequence extracted from NCBI backbone (NCBIN:132811, NCBI:132813)
C:Superfamily: erythropoietin receptor; cytokine receptor; glycoprotein; transmembrane protein
C:Keywords: cytokine receptor; glycoprotein; transmembrane protein
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-507/Product: erythropoietin receptor #status predicted <MAT>
F:25-249/Domain: extracellular #status predicted <EXT>
F:52-338/Domain: cytokine receptor homology <CRS>
F:250-271/Domain: transmembrane #status predicted <TM>
F:272-507/Domain: intracellular #status predicted <INT>
F:75/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 82.2%; Score 981.5; DB 1; Length 507;
Best Local Similarity 82.7%; Pred. No. 2.9e-82;
Matches 186; Conservative 15; Mismatches 23; Indels 1; Gaps 1;

QY 1 APPNPDPKFEKSKAALLAARGPEELCTERLEDCVCFWEERASAGVGNYSFYOLE 60

Query Match 80.9%; Score 966.5; DB 2; Length 265;
Best Local Similarity 82.9%; Pred. NO. 3e-81;
Matches 184; Conservative 13; Mismatches 24; Indels 1; Gaps 1;

OY 1 APPNLPDPKRESKAALLAAGPELLCETRLDLYOCFWEAAASAGCPGPNVSFOLE 60
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 25 APSPSLPPPKESKALLASRGSEELLCTQRLIEDLVCFWEEAANSNG - FNYSFOLE 83
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 61 DEPMKLCLHQAPTARGAVRWCSLPTADTSSFPVLELRVTAAAGAPRYHRVITINEVYL 120
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 84 GESRSKSCHLAQPVRGSMRFWCSLPTADTSSFPVLELQVTEAGSPRYHRITINEVYL 143
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 121 LDAPVGLIARLADESGHYVLMPLPETPMTSHLREYDVASAGNAGSVOREILEGRTE 180
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 144 LDAPVGLIARLAAREBSHVYLMPLPPGAPMTTHIRYEYDVASGNRAGGTORVEVLEGRT 203
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 181 CVLSNLNGRTRYTFAYVARMAEPSTFGFWMSAMSEPVSLTPSD 225
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 204 CVLSNLNGRTRYTFAYVARMAEPSTFGFWMSAMSEPASILTASDL 248
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 4
S14081 erythropoietin receptor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S14081 | Y9653
R:Kuramochi, S.; Ikawa, Y.; Todokoro, K.
J. Mol. Biol. 216, 567-575, 1990
A:title: Characterization of murine erythropoietin receptor genes.
A:Reference number: S13249; MUID:91080149
A:Accession: S14081
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-265 <KUR>
R:Lacombe, C.; Chetellen, S.; Lemarchandel, V.; Mayeux, P.; Romeo, P.
J. Biol. Chem. 266, 6952-6956, 1991
A:title: Spleen focus-forming virus long terminal repeat insertional activation of the p
A:Reference number: I49653; MUID:91201346
A:Accession: I49653
A>Status: preliminary; translated from GB/EMBL/DBD
A:Molecule type: DNA
A:Residues: 1-24 <RES>
A:Cross-references: GB:M62360; NID:g193199; PIDN:AAA37582.1; PID:g193200
C:Superfamily: erythropoietin receptor; cytokine receptor homology
C:Keywords: cytokine receptor; transmembrane protein
F:52-238/Domain: cytokine receptor homology <CRS>

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A>Title: Murine c-mpl; a member of the hematopoietic growth factor receptor superfamily
A:Reference number: S35316; MUID:93327753
A:Accession: S35317
A:Molecule type: mRNA
A:Residues: 1-625 <SKO>
A:Cross-references: EMBL:L22649; NID:g94725; PIDN:CAM80365.1; PID:g94726
A:Accession: S35316
A:Molecule type: DNA
A:Residues: 1-70 <SKW>
A:Cross-references: EMBL:Z22657
C:Keywords: alternative splicing; cytokine receptor; glycoprotein; transmembrane protein
F:1-25/Domain: signal sequence #status predicted <SIG>
F:26-625/Product: hematopoietic growth factor receptor #status predicted <MAT>
F:26-482/Domain: extracellular #status predicted <Ext>
F:261-265/Region: WGXWS motif
F:463-504/Domain: transmembrane #status predicted <TM>
F:505-625/Domain: intracellular #status predicted <INT>
F:113,117,178,349/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match      17.2%; Score 205; DB 2; Length 625;
Best Local Similarity 25.9%; Pred. No. 8.1e-11;
Matches    66; Conservative   29; Mismatches 112; Indels   48; Gaps     7;

OY      13 SKAALLARGPBELICTERLEDLVCWEENASAGVGPGNTSFSYQLEDEPWKICRLHQ 72
       1 : - - - - - | - - - - - ||| ||| : - - - - - | - - - - - | : - - - - -
Db      25 SQDFLLALGTETPLNCFSQTEDLTCEWDEEAA--PSGTYQLLYAVRGEKPACPLYSQ 82
       1 : - - - - - | - - - - - ||| ||| : - - - - - | - - - - - | : - - - - -

OY      73 PTARGAVFWCSLPTAD--TSSEVPLELRVTAA--GAPRIHRYIHINEVILLDAVGLVAR 130
       83 SVPTFGTGYTCVCFPRQDEVRLFEPFLHWKNVSLNOTLIQVLVDSDGLPAPPVITAK 142
       8 : - - - - - | - - - - - | - - - - - | - - - - - | - - - - - | - - - - -

OY      131 LADESGHYLVKW-LPPPETP--MTSHIRYEVDVSAGNGAGSVGRVEILEGRT----- 179
       1 : - - - - - | - - - - - | - - - - - | - - - - - | - - - - - | - - - - -
Db      143 GGSQGQELQHMEAPAPRPISDFLRHELRYGPTDSSNMATPV--IQLLSTFTCCPTLMIP 200
       1 : - - - - - | - - - - - | - - - - - | - - - - - | - - - - - | - - - - -

OY      180 -----ECVLSNLRGTRTYTFVVRARMAEPSFGGF 208
       1 : - - - - - | - - - - - | - - - - - | - - - - - | - - - - - | - - - - -
Db      201 NPVPYLDPPCVHPHTASQPHGPAPEFLTWKGSCSLVGLQASKSYWLRLRSQPDGVSLRGS 260
       1 : - - - - - | - - - - - | - - - - - | - - - - - | - - - - - | - - - - -

OY      209 WSANSEPYSILTPSD 223
       1 : - - - - - | - - - - - | - - - - - | - - - - - | - - - - - | - - - - -
Db      261 WGPMSFPVTDLPDG 275

RESULT
6      S37622
Proto-oncogene - mouse
C:Species: Mus musculus (house mouse)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
C:Accession: S37622
R:Viigon, I.; Florindo, C.; Fichelson, S.; Guenet, J.L.; Mattei, M.G.; Souyri, M.; Cos
OncoGene 8, 2607-2615, 1993
A>Title: Characterization of the murine Mpl proto-oncogene, a member of the hematopoi
A:Reference number: S37622; MUID:93390934
A:Accession: S37622
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-626 <VTG>
A:Cross-references: EMBL:X73677; NID:g404318; PIDN:CAA52031.1; PID:g404319

Query Match      16.6%; Score 198; DB 2; Length 626;
Best Local Similarity 24.7%; Pred. No. 3.6e-10;
Matches    65; Conservative   30; Mismatches 112; Indels   56; Gaps     7;

OY      13 SKAALLARGPDELICTERLEDLVCWEENASAGVGPGNTSFSYQLEDEPWKICRLHQ 72
       1 : - - - - - | - - - - - ||| ||| : - - - - - | - - - - - | : - - - - -
Db      18 SQDFLLALGTETPLNCFSQTEDLTCEWDEEAA--PSGTYQLLYAVRGEKPACPLYSQ 75
       1 : - - - - - | - - - - - ||| ||| : - - - - - | - - - - - | : - - - - -

OY      73 PTARGAVFWCSLPT-ADTSSFVPLELRVTAA--GAPRIHRYIHINEVILLDAVGLVAR 130

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[illegible]

Query March 15.5% Score 185; DB 2; Length 579;
Best Local Similarity 24.5%; Pred. No. 5e-09;
Matches 67; Conservative 30; Mismatches 117; Indels 60; Gaps 9;

QY 3 PPNTDPPEESKAAALLARCPHEELICFTEERLEDIVCFWEAASAGVGGNYSFYOLEDE 62
| | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 17 PQNL--AQVSSQDVSLLASDSSEPLKCFSTRFEEDLCFFNDEEBA--PSGTQLLAYRRE 72

QY 63 PWKLCRLHQAAPTARGAVRFWCSLP-TADTSSFVPLELRY-TAASGAPRYHRVHIINEVYL 120
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 73 KPRACPLSSQSMPHGRTRYVCQFPDQEVRLEFFLHWKNVFLNQTRQVLFFVDISGL 132

QY 121 LDAPGVLAIRLADESCHVYLRN-LPPPETPMTSHIRYV-----DVSGNGAGSVQRVE- 173
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 133 PAPSIIRKAMGSQPGELOISWEEPAE--ISDFELRYELRGPRDPKNSFTGPVIQLIAT 190

QY 174 -----ILBERTCYLSNLGR 189
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

Db 191 ETCCPALORPHSASALDOSPCAQTPTMWDGPKOTSPSRSAALTAEGGS-CLISGLPG 249

QY 190 TRTYFAVARARAEPSPGFMSAMSEPVSLTPSD 223
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 250 NSYMLQLRSEPDDGISLGSGMGSKSLPYTDLPDG 283

RESULT 8
A45266
MPV-P protein precursor - human
C:Species: Homo sapiens (man)
C>Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 05-Nov-1999
C:Accession: A45266
R:Viigon, I.; Morron, J.P.; Cocault, L.; Mitjavila, M.T.; Tambourin, P.; Gisselbrecht, S.
Proc. Natl. Acad. Sci. U.S.A. 89, 5640-5644, 1992
A>Title: Molecular cloning and characterization of MPV, the human homolog of the v-mpl c-
A:Reference number: A45266; MUID:92302297
A:Accession: A45266
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-635 <VTG>
A:Cross-references: GB:I90102; NID:g184260; PIDN:AAA69971.1; PID:g184261

C;Keywords: transmembrane protein

Query Match	15.5%:	Score 185:	DB 2:	Length 635:
Best Local Similarity	24.5%:	Pred. No.5.7e-09:		
Matches	67:	Conservative	30:	Mismatches 117: Indels 60: Gaps 9:
QY	3	PENLDPPKFEESAAALTAARGPEELICTFERLEDVLCFMEEAASAGVCGNYSFSYOLEDE	62	
		: : : : : : : : : : : : : : : : : : : : : : : : :		
DB	17	PQNL--AQVSSDDVSLASDSDEPLKCFSTFEDDLTCFMEDEEAA--PSTGYLLAYPRE	72	
		: : : : : : : : : : : : : : : : : : : : : : : : :		
QY	63	PWKLCRLQAPATARGAVRWCSLP-TADTSSFVPLELRY-TAASGAPRHRVHINIEVYL	120	
		: : : : : : : : : : : : : : : : : : : : : : : : :		
DB	73	KPRACPLESQSMHFGHTGYVCOFPDQGEVRLRFLPLHMWKNNFLMQTRQVRLPFVDSGL	132	
		: : : : : : : : : : : : : : : : : : : : : : : : :		
QY	121	LDAPVGLVARLADESGHVYLKW-LPPETTPMTSHIRYEV-----DVSAGNGAGSYQRYE-	173	
		: : : : : : : : : : : : : : : : : : : : : : : : :		
DB	133	PAPFIIIRKMGSGQCGELQISWEEPAPE--ISDFLRLEYRVPGRDPKKNSTGPTVIQTLAT	190	
		: : : : : : : : : : : : : : : : : : : : : : : : :		
QY	174	-----ILBGRTEVLNSLNGR	189	
		: : : : : : : : : : : : : : : : : : : : : : : : :		
DB	191	ETCCPALQRPHSASALDOSPCAQPTPMQDQPKQTSRHSASALTAEEGGS-CLISGLQPG	249	
		: : : : : : : : : : : : : : : : : : : : : : : : :		
QY	190	TRTYFAVRARARAAEPSEGGFMSAMSEVSLTPSPSD	223	
		: : : : : : : : : : : : : : : : : : : : : : : : :		
DB	250	NSYWLQLRSEPDGILSGGSGWSLSLPVTVDLEGD	283	
		: : : : : : : : : : : : : : : : : : : : : : : : :		

RESULT 9
145971
prolactin receptor - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text-change 28-Jul-2000
C:Accession: 145971
R:Scott, P.; Kessler, M.A.; Schuler, L.A.
Mol. Cell. Endocrinol. 89, 47-58, 1992
A:Title: Molecular cloning of the bovine prolactin receptor and distribution of prolactin receptor mRNA
A:Reference number: 145971; MUID:93246019
A:Accession: 145971
A:Status: Preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-581 <SCO>
A:Cross-references: GB:102549; NID:g163617; PIDN:AAA51417.1; PID:g163618
C:genetics:
A:Gene: PRLR
C:Superfamily: cytokine receptor homology
;36-221/Domain: cytokine receptor homology <CRS>

[illegible]

RESULT 10
A30304
prolactin receptor 2 precursor - rabbit

N:Alternate names: prolactin receptor, mammary gland
C:Species: *Oryctolagus cuniculus* (domestic rabbit)
C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 28-Jul-2000
C:Accession: A30304; A60380
R:Entry: M.; Jolicoeur, C.; Levi-Meynreis, C.; Dusanter-Fourt, I.; Petridou, B.; Boulton,
Proc. Natl. Acad. Sci. U.S.A. 86, 2112-2116, 1989
A:Title: Identification and sequence analysis of a second form of prolactin receptor by
A:Reference number: A30304; MUID:89184578
A:Accession: A30304
A:Molecule type: mRNA
A:Residues: 1-616 <EDED>
A:Cross-references: GB:J04510; NID:g165669; PIDD:AAA31457.1; PID:g165670
R:Waters, M.J.; Spencer, S.A.; Hamlin, G.; Henzel, W.J.; Wood, W.I.
Int. J. Biochem. 22, 1089-1095, 1990
A:Title: Purification and partial sequence of the rabbit mammary gland prolactin receptor
A:Reference number: A60380; MUID:91146782
A:Accession: A60380
A:Molecule type: protein
A:Residues: 41-58,'X',60-66,'90'-93,'X',95-96,'X',98-103,'X',105,'NX',108;150-164,'XX',167
A:Note: The amino end of the mature protein was blocked
C:Superfamily: cytokine receptor homology
C:Keywords: blocked amino end; glycoprotein; transmembrane protein
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-616/Product: prolactin receptor 2 #status predicted <MAT>
F:36-221/Domain: cytokine receptor homology <CRS>
F:23-238/Domain: transmembrane #status predicted <TM>
F:59,104,132,347,389,411/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match	12.48;	Score 148;	DB 2;	Length 616;
Best Local Similarly	24.5%;	Pred. No. 1.4e-05;		
Matches 57; Conservative	31;	Mismatches 103;	Indels 42;	Gaps 11;

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Oy 3 PPNLPDPKFEESKALLIARGEEELLCTERIEDLVCTWEERASAGVCPGNYSTSYQLEDE 62
    11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
Db 27 PPGKP-----FIFKRSKP-----ETFCQMRGADGGL-PTNYTLYHNEGE 69
    11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
Oy 63 PFKLCRLCHQAPTLAAGVAVFMSCLPTADSSPFLLELVTAAS-----GAPRYHRVYHIN 116
    11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
Db 70 -----TTHCECDYRTGGPNSCFESKKTSTWTTIITVYNAINOMGSSVSDPKY--VDVT 122
    11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
Oy 117 EVLLIDAFVGL--VARLADESGHVILRWLPEPTPMTS--HRYEVVDASAGASGYQ 170
    11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
Db 123 YIVEDDPVPVNLTELEKHPEDRKPIYAKWKLPPTLVDRVSGMLTLQYIIRLKPCKAA--EM 180
    11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
Oy 171 RVELLEGTECEVLSNLKGRRTYTTAVARRAAEPGFGWASMEPVSLLTPSD 223
    11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
Db 181 ETHFAGOOTQRIKLSLTPGQKYLQVQVCK--PDH-GFWASWSESSIQIPND 229
    11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11

```

RESULT 11

prolactin receptor precursor - chicken
C:Species: Gallus gallus (chicken)
C:Date: 30-Sep-1993 #sequence.revision 30-Sep-1993 #text.change 28-Jul-2000
C:Accession: J01655
R:Tanaka, M.; Maeda, K.; Okubo, T.; Nakashima, K.
Biochem. Biophys. Res. Commun. 188, 490-496, 1992
A:Title: Double antenna structure of chicken prolactin receptor deduced from the cDNA seq
A:Reference number: J01655; MUID:93075121
A:Accession: J01655
A:Molecule type: mRNA
A:Residues: 1-831 <TAN>
A:Cross-references: DDBJ:DJ13154; NID:9222848; PIDD:BA002439.1; PTD:9222849
A:Experimental source: kidney
A:Superfamily: cytokine receptor homology
C:Keywords: glycoprotein; transmembrane protein
E:1-33/Domain: signal sequence #status predicted <IG>
E:34-83/Product: prolactin receptor #status predicted <MAT>
E:36-219/Domain: cytokine receptor homology <CRS1>
E:239-435/Domain: cytokine receptor homology <CRS2>
E:439-462/Domain: transmembrane #status predicted <TM>
E:559-921,100,112,132,562,303,315,335,647,701,800/Binding site: carbohydrate (asn) (covale

Query Match	12.1%	Score 144.5;	DB 2;	Length 831;
Best Local Similarity	23.5%;	Pred. No. 4.2e-05;		
Matches 55; Conservative	33;	Mismatches 103;	Indels 43;	Gaps 11;

[illegible]

RESULT 12
I50455

C:Species: *Columba livia* (domestic pigeon)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 28-Jul-2000
C:Accession: I50455
R:Chen, X.; Horseman, N.D.
Endocrinology 135, 269-276, 1994
A:Title: Cloning, expression, and mutational analysis of the pigeon prolactin receptor
A:Reference number: I50455; MUID:94283267
A:Accession: I50455
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-830 <CHE>
A:Cross-references: EMBL:U07694; NID:g466381; PIDN:AAA20646.1; PID:g466382
C:Superfamily: cytokine receptor homology
F:36-220/Domain: cytokine receptor homology <CRS1>
F:240-426/Domain: cytokine receptor homology <CRS2>

Query Match	11.48;	Score 136.5;	DB 2;	Length 830;
Best Local Similarity	23.28;	Pred. No. 0.00023;		
Matches 55; Conservative	33;	Mismatches 104;	Indels 45;	Gaps 11;

```

QY      4 PNLDDPKFESKAAALTAARGPEELLCFTERLEDLVCFWEEASAGVGBGNYSFSYQLDEEP 63
      11 - - - - - 1111 - - - - - 1111 - - - - - 1111 - - - - -
Db      226 PNGNSP--PEKPTIICRSPK-----ETPFCWKKPGSDGG-HPTNYTLILSKEGEE 27

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04
QY[illegible]

RESULT 13

559405
 prolactin receptor short form S1b precursor, breast cancer cells T-47D - human
 C|Species: Homo sapiens (man)
 C|Date: 01-Feb-2002 #sequence-revision 01-Feb-2002 #text-change 01-Feb-2002
 C|Accession: B59405
 R|Hu, Z.Z.; Meng, J.; Dufau, M.L.
 J. Biol. Chem. 276, 41086-41094, 2001
 #Title: Isolation and characterization of two novel forms of the human prolactin

A:Reference number: A59405; MUID:21538812; PMID:11518703
A:Accession: B59405
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-288 <HUI>
A:Cross-References: GB:AF214012; PIDN:AF214012.1
C:Genetics:
A:Gene: GDB:PRLR
A:Cross-References: GDB:120315; OMIM:176761
A:Map position: 5p13.3-5p13.1
C:Superfamily: cytokine receptor homology
C:Keywords: glycoprotein, transmembrane protein
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-288/Product: prolactin receptor, short form S1b #status predicted <MAT>
F:36-221/Domain: cytokine receptor homology <CRS>
F:59,104,233/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 10.7%; Score 128; DB 2; Length 288;
Best Local Similarity 23.8%; Pred. No. 0.00035;
Matches 50; Conservative 33; Mismatches 107; Indels 20; Gaps 9;

OY 23 PEEILCFETRLIEDVCFWEAASAGVPGNYSFVQLDEDEPMKLCRLHQAPFARGAVRFW 82
DB 31 PETFKCRSPNKEFTTCWMPRGTDGGL-PTNYSILTYHREGE---TLMHCPCDYITGGPNS 85
OY 83 CSLPTADTSSFYPLELRVTAAS--GAPRYHRV-IHINEVLLDAPVGL--VARLADESG 136
DB 86 CHFGKQYTSMMRTYIMVNATNMGSSFSDELVDVITYVQDPPELAVEVQKPEDRKP 145
OY 137 HVALRMLPPPEPMTS---HIREVDVSANGAGSVQRYEILGRTCEVLSNLRGTRTY 193
DB 146 YLMIKWSPPTLLDLKGTWFTLTYEIRLKEPKAA--EMEIHFAGOQTEFKILSLHPQKYL 203
OY 194 FAVRARMAPSPFGFWSAMSEPSVSLITPSD 223
DB 204 VOVRCK---PDH-GYWSAMSPATFIQIPSD 229

RESULT 14
A59405
prolactin receptor short form S1a precursor, breast cancer cells T-47D - human
C:Species: Homo sapiens
C:Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
C:Accession: A59405
R:Hu, Z. Z.; Meng, J.; Dufau, M. L.
J. Biol. Chem. 276, 41086-41094, 2001
A:Title: Isolation and characterization of two novel forms of the human prolactin receptor
A:Reference number: A59405; MUID:21538812; PMID:11518703
A:Accession: A59405
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-376 <HUI>
A:Cross-References: GB:AF214012; PIDN:AF214012.1
C:Genetics:
A:Gene: GDB:PRLR
A:Cross-References: GDB:120315; OMIM:176761
A:Map position: 5p13.3-5p13.1
C:Superfamily: cytokine receptor homology
C:Keywords: glycoprotein, transmembrane protein
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-288/Product: prolactin receptor, short form S1a #status predicted <MAT>
F:36-221/Domain: cytokine receptor homology <CRS>
F:59,104,233/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 10.7%; Score 128; DB 2; Length 376;
Best Local Similarity 23.8%; Pred. No. 0.0005;
Matches 50; Conservative 33; Mismatches 107; Indels 20; Gaps 9;

OY 23 PEEILCFETRLIEDVCFWEAASAGVPGNYSFVQLDEDEPMKLCRLHQAPFARGAVRFW 82
DB 31 PETFKCRSPNKEFTTCWMPRGTDGGL-PTNYSILTYHREGE---TLMHCPCDYITGGPNS 85

OY 83 CSLPTADTSSFYPLELRVTAAS--GAPRYHRV-IHINEVLLDAPVGL--VARLADESG 136
DB 86 CHFGKQYTSMMRTYIMVNATNMGSSFSDELVDVITYVQDPPELAVEVQKPEDRKP 145
OY 137 HVALRMLPPPEPMTS---HIREVDVSANGAGSVQRYEILGRTCEVLSNLRGTRTY 193
DB 146 YLMIKWSPPTLLDLKGTWFTLTYEIRLKEPKAA--EMEIHFAGOQTEFKILSLHPQKYL 203
OY 194 FAVRARMAPSPFGFWSAMSEPSVSLITPSD 223
DB 204 VOVRCK---PDH-GYWSAMSPATFIQIPSD 229

RESULT 15
A40144
prolactin receptor long form precursor, hepatoma and breast cancer cells - human
C:Species: Homo sapiens (man)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 01-Dec-2000
C:Accession: A40144; A57018
R:Boutin, J. M.; Edey, M.; Shirota, M.; Jolicoeur, C.; Lesueur, L.; Ali, S.; Gould, D
Mol. Endocrinol. 3, 1455-1461, 1989
A:Title: Identification of a cDNA encoding a long form of prolactin receptor in human
A:Reference number: A40144; MUID:90114212
A:Accession: A40144
A:Molecule type: mRNA
A:Residues: 1-622 <BOU>
A:Cross-References: GB:M31661; NID:9190361; PIDN:AAA60174.1; PID:9190362
R:Fuh, G.; Wells, J. A.
J. Biol. Chem. 270, 13133-13137, 1995
A:Title: Prolactin receptor antagonists that inhibit the growth of breast cancer cell
A:Reference number: A57018; MUID:95286597
A:Accession: A57018
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 25-228, 'AW' <RES>
A:Cross-References: GB:S78505; NID:9999114; PIDN:AAB34470.1; PID:9999115
C:Genetics:
A:Gene: GDB:PRLR
A:Cross-References: GDB:120315; OMIM:176761
A:Map position: 5p13.3-5p13.1
C:Superfamily: cytokine receptor homology
C:Keywords: glycoprotein, transmembrane protein
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-622/Product: prolactin receptor, long form #status predicted <MAT>
F:36-221/Domain: cytokine receptor homology <CRS>
F:59,104,233/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 10.7%; Score 128; DB 2; Length 622;
Best Local Similarity 23.8%; Pred. No. 0.00095;
Matches 50; Conservative 33; Mismatches 107; Indels 20; Gaps 9;

OY 23 PEEILCFETRLIEDVCFWEAASAGVPGNYSFVQLDEDEPMKLCRLHQAPFARGAVRFW 82
DB 31 PETFKCRSPNKEFTTCWMPRGTDGGL-PTNYSILTYHREGE---TLMHCPCDYITGGPNS 85
OY 83 CSLPTADTSSFYPLELRVTAAS--GAPRYHRV-IHINEVLLDAPVGL--VARLADESG 136
DB 86 CHFGKQYTSMMRTYIMVNATNMGSSFSDELVDVITYVQDPPELAVEVQKPEDRKP 145
OY 137 HVALRMLPPPEPMTS---HIREVDVSANGAGSVQRYEILGRTCEVLSNLRGTRTY 193
DB 146 YLMIKWSPPTLLDLKGTWFTLTYEIRLKEPKAA--EMEIHFAGOQTEFKILSLHPQKYL 203
OY 194 FAVRARMAPSPFGFWSAMSEPSVSLITPSD 223
DB 204 VOVRCK---PDH-GYWSAMSPATFIQIPSD 229

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